

## SEQUENCE LISTING

<110> Ajinomoto Co., Inc.

<120> Inosine producing bacterium belonging to the genus  
Bacillus and method for producing inosine

<130> US-108

<150> JP 2003-37760

<151> 2003-02-17

<160> 16

<170> PatentIn Ver. 2.0

<210> 1

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 1

ctcaagcttg aagttgcgat gatcaaaa

28

<210> 2

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

<400> 2  
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<210> 3  
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<220>  
<223> Description of Artificial Sequence: primer

<400> 3  
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<210> 4  
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<223> Description of Artificial Sequence: primer

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<210> 5  
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<223> Description of Artificial Sequence: primer

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<223> Description of Artificial Sequence: primer

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ctcaagctta tggtttccag accatcgact 30

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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33

<210> 10

<211> 33

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

<400> 10

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33

<210> 11

<211> 1200

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (259)..(1113)

<400> 11

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tgtaaatgag cgggagcggc ccgacagtgt ttggactggt tcagtatgag tcgaaggtgc 120  
agagaattta taacgggtta agaggcttct gcgatcaagt ttatgcggtg agaatgatcg 180  
gcgaacagaa cgctcttgat taaatccgta tgtaagtta tattgatctt aaaatattcg 240  
gattttgggg gtgagttc atg aag ttt cgt cgc agc ggc aga ttg gtg gac 291

Met	Lys	Phe	Arg	Arg	Ser	Gly	Arg	Leu	Val	Asp						
1					5				10							
tta	aca	aat	tat	ttg	tta	acc	cat	cgc	cac	gag	tta	ata	cgc	cta	acc	339
Leu	Thr	Asn	Tyr	Leu	Leu	Thr	His	Pro	His	Glu	Leu	Ile	Pro	Leu	Thr	
	15					20					25					
ttt	ttc	tct	gag	cgg	tat	gaa	tct	gca	aaa	tca	tcg	atc	agt	gaa	gat	387
Phe	Phe	Ser	Glu	Arg	Tyr	Glu	Ser	Ala	Lys	Ser	Ser	Ile	Ser	Glu	Asp	
	30					35					40					
tta	aca	att	att	aaa	caa	acc	ttt	gaa	cag	cag	ggg	att	ggt	act	ttg	435
Leu	Thr	Ile	Ile	Lys	Gln	Thr	Phe	Glu	Gln	Gln	Gly	Ile	Gly	Thr	Leu	
	45					50					55					
ctt	act	gtt	ccc	gga	gct	gcc	gga	ggc	gtt	aaa	tat	att	cgc	aaa	atg	483
Leu	Thr	Val	Pro	Gly	Ala	Ala	Gly	Gly	Val	Lys	Tyr	Ile	Pro	Lys	Met	
	60					65				70						
aag	cag	gct	gaa	gct	gaa	gag	ttt	gtg	cag	aca	ctt	gga	cag	tcg	ctg	531
Lys	Gln	Ala	Glu	Ala	Glu	Glu	Phe	Val	Gln	Thr	Leu	Gly	Gln	Ser	Leu	
		80							85					90		
gca	aat	cct	gag	cgt	atc	ctt	cgc	ggc	ggt	tat	gta	tat	tta	acg	gat	579
Ala	Asn	Pro	Glu	Arg	Ile	Leu	Pro	Gly	Gly	Tyr	Val	Tyr	Leu	Thr	Asp	
	95								100					105		
atc	tta	gga	aag	cca	tct	gta	ctc	tcc	aag	gta	ggg	aag	ctg	ttt	gct	627
Ile	Leu	Gly	Lys	Pro	Ser	Val	Leu	Ser	Lys	Val	Gly	Lys	Leu	Phe	Ala	
	110								115					120		
tcc	gtg	ttt	gca	gag	cgc	gaa	att	gat	gtt	gtc	atg	acc	gtt	gcc	acg	675
Ser	Val	Phe	Ala	Glu	Arg	Glu	Ile	Asp	Val	Val	Met	Thr	Val	Ala	Thr	
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aaa	ggc	atc	cct	ctt	gcg	tac	gca	gct	gca	agc	tat	ttg	aat	gtg	cct	723
Lys	Gly	Ile	Pro	Leu	Ala	Tyr	Ala	Ala	Ala	Ser	Tyr	Leu	Asn	Val	Pro	
	140					145					150				155	
gtt	gtg	atc	gtt	cgt	aaa	gac	aat	aag	gta	aca	gag	ggc	tcc	aca	gtc	771
Val	Val	Ile	Val	Arg	Lys	Asp	Asn	Lys	Val	Thr	Glu	Gly	Ser	Thr	Val	
		160							165					170		
agc	att	aat	tac	gtt	tca	ggc	tcc	tca	aac	cgc	att	caa	aca	atg	tca	819
Ser	Ile	Asn	Tyr	Val	Ser	Gly	Ser	Ser	Asn	Arg	Ile	Gln	Thr	Met	Ser	
	175								180					185		
ctt	gcg	aaa	aga	agc	atg	aaa	acg	ggt	tca	aac	gta	ctc	att	att	gat	867

Leu Ala Lys Arg Ser Met Lys Thr Gly Ser Asn Val Leu Ile Ile Asp  
 190 195 200  
 gac ttt atg aaa gca ggc ggc acc att aat ggt atg att aac ctg ttg 915  
 Asp Phe Met Lys Ala Gly Gly Thr Ile Asn Gly Met Ile Asn Leu Leu  
 205 210 215  
 gat gag ttt aac gca aat gtg gcg gga atc ggc gtc tta gtt gaa gcc 963  
 Asp Glu Phe Asn Ala Asn Val Ala Gly Ile Gly Val Leu Val Glu Ala  
 220 225 230 235  
 gaa gga gta gat gaa cgt ctt gtt gac gaa tat atg tca ctt ctt act 1011  
 Glu Gly Val Asp Glu Arg Leu Val Asp Glu Tyr Met Ser Leu Leu Thr  
 240 245 250  
 ctt tca acc atc aac atg aaa gag aag tcc att gaa att cag aat ggc 1059  
 Leu Ser Thr Ile Asn Met Lys Glu Lys Ser Ile Glu Ile Gln Asn Gly  
 255 260 265  
 aat ttt ctg cgt ttt ttt aaa gac aat ctt tta aag aat gga gag aca 1107  
 Asn Phe Leu Arg Phe Phe Lys Asp Asn Leu Leu Lys Asn Gly Glu Thr  
 270 275 280  
 gaa tca tgacaaaagc agtccacaca aaacatgccc cagcggcaat cgggccttat 1163  
 Glu Ser  
 285  
 tcacaaggga ttatcgtcaa caatatgttt tacagct 1200

<210> 12

<211> 285

<212> PRT

<213> *Bacillus subtilis*

<400> 12

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 Tyr Glu Ser Ala Lys Ser Ser Ile Ser Glu Asp Leu Thr Ile Ile Lys  
 35 40 45  
 Gln Thr Phe Glu Gln Gln Gly Ile Gly Thr Leu Leu Thr Val Pro Gly

50	55	60
Ala Ala Gly Gly Val Lys Tyr Ile Pro Lys Met Lys Gln Ala Glu Ala		
65	70	75
Glu Glu Phe Val Gln Thr Leu Gly Gln Ser Leu Ala Asn Pro Glu Arg		
85	90	95
Ile Leu Pro Gly Gly Tyr Val Tyr Leu Thr Asp Ile Leu Gly Lys Pro		
100	105	110
Ser Val Leu Ser Lys Val Gly Lys Leu Phe Ala Ser Val Phe Ala Glu		
115	120	125
Arg Glu Ile Asp Val Val Met Thr Val Ala Thr Lys Gly Ile Pro Leu		
130	135	140
Ala Tyr Ala Ala Ala Ser Tyr Leu Asn Val Pro Val Val Ile Val Arg		
145	150	155
Lys Asp Asn Lys Val Thr Glu Gly Ser Thr Val Ser Ile Asn Tyr Val		
165	170	175
Ser Gly Ser Ser Asn Arg Ile Gln Thr Met Ser Leu Ala Lys Arg Ser		
180	185	190
Met Lys Thr Gly Ser Asn Val Leu Ile Ile Asp Asp Phe Met Lys Ala		
195	200	205
Gly Gly Thr Ile Asn Gly Met Ile Asn Leu Leu Asp Glu Phe Asn Ala		
210	215	220
Asn Val Ala Gly Ile Gly Val Leu Val Glu Ala Glu Gly Val Asp Glu		
225	230	235
Arg Leu Val Asp Glu Tyr Met Ser Leu Leu Thr Leu Ser Thr Ile Asn		
245	250	255
Met Lys Glu Lys Ser Ile Glu Ile Gln Asn Gly Asn Phe Leu Arg Phe		
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Phe Lys Asp Asn Leu Leu Lys Asn Gly Glu Thr Glu Ser		
275	280	285

<210> 13

<211> 1490

<212> DNA

<213> *Bacillus subtilis*

<220>

<221> CDS

<222> (101).. (1393)

<400> 13

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                                     Met Ser Ser Val Val
                                     1           5
gta gta ggt acg caa tgg ggc gat gaa gga aaa ggt aaa att aca gat 163
Val Val Gly Thr Gln Trp Gly Asp Glu Gly Lys Gly Lys Ile Thr Asp
                10                15                20
ttc cta tca gaa aat gca gaa gtg atc gcc cgt tat caa ggc gga aat 211
Phe Leu Ser Glu Asn Ala Glu Val Ile Ala Arg Tyr Gln Gly Gly Asn
                25                30                35
aac gca ggg cat aca atc aag ttt gac gga atc aca tat aag ctt cac 259
Asn Ala Gly His Thr Ile Lys Phe Asp Gly Ile Thr Tyr Lys Leu His
                40                45                50
tta atc ccg tct gga att ttc tat aag gat aaa acg tgt gta atc gga 307
Leu Ile Pro Ser Gly Ile Phe Tyr Lys Asp Lys Thr Cys Val Ile Gly
                55                60                65
aac gga atg gtt gta gat ccg aaa gca tta gtc aca gag ctt gcg tat 355
Asn Gly Met Val Val Asp Pro Lys Ala Leu Val Thr Glu Leu Ala Tyr
                70                75                80                85
ctt cat gag cgc aac gtg agt aca gat aac ctg aga atc agc aac aga 403
Leu His Glu Arg Asn Val Ser Thr Asp Asn Leu Arg Ile Ser Asn Arg
                90                95                100
gct cac gtc att ctg ccg tat cat ttg aaa ttg gat gaa gtg gaa gaa 451
Ala His Val Ile Leu Pro Tyr His Leu Lys Leu Asp Glu Val Glu Glu
                105                110                115
gag cgt aaa ggg gct aac aag atc ggc aca acg aaa aaa gga atc ggc 499
Glu Arg Lys Gly Ala Asn Lys Ile Gly Thr Thr Lys Lys Gly Ile Gly
                120                125                130
cct gct tac atg gat aaa gca gcc cgc atc gga att cgc atc gcg gat 547
Pro Ala Tyr Met Asp Lys Ala Ala Arg Ile Gly Ile Arg Ile Ala Asp
                135                140                145
ctg tta gac cgt gac gcg ttt gcg gaa aag ctt gag cgc aat ctt gaa 595
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Ile Cys Val Ala Tyr Arg Tyr Lys Gly Glu Ile Ile Glu Glu Phe Pro	
345 350 355	
gca agt ctt aag gca ctt gct gaa tgt gag ccg gta tat gaa gaa atg	1219
Ala Ser Leu Lys Ala Leu Ala Glu Cys Glu Pro Val Tyr Glu Glu Met	
360 365 370	
ccg ggc tgg act gag gat att aca ggt gcg aag agc ttg agc gag ctt	1267
Pro Gly Trp Thr Glu Asp Ile Thr Gly Ala Lys Ser Leu Ser Glu Leu	
375 380 385	
ccg gaa aat gcg cgc cat tat ctt gag cgt gtg tct cag ctg aca ggc	1315
Pro Glu Asn Ala Arg His Tyr Leu Glu Arg Val Ser Gln Leu Thr Gly	
390 395 400 405	
att ccg ctt tct att ttc tct gtc ggt cca gac cgc tca caa aca aat	1363
Ile Pro Leu Ser Ile Phe Ser Val Gly Pro Asp Arg Ser Gln Thr Asn	
410 415 420	
gtc ctt cgc agt gtg tac cgt gcg aac taa atagaatatg tctgcaagcc	1413
Val Leu Arg Ser Val Tyr Arg Ala Asn	
425 430	
cctatttaag gggcttgttt tttgtttgaa agccgcataat aagtttgtct gagaaaaaa	1473
tatgaaaaaa aaccaaa	1490

<210> 14

<211> 430

<212> PRT

<213> Bacillus subtilis

<400> 14

Met Ser Ser Val Val Val Val Gly Thr Gln Trp Gly Asp Glu Gly Lys	
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Tyr Gln Gly Gly Asn Asn Ala Gly His Thr Ile Lys Phe Asp Gly Ile	
35 40 45	
Thr Tyr Lys Leu His Leu Ile Pro Ser Gly Ile Phe Tyr Lys Asp Lys	
50 55 60	
Thr Cys Val Ile Gly Asn Gly Met Val Val Asp Pro Lys Ala Leu Val	
65 70 75 80	

Thr Glu Leu Ala Tyr Leu His Glu Arg Asn Val Ser Thr Asp Asn Leu  
 85 90 95  
 Arg Ile Ser Asn Arg Ala His Val Ile Leu Pro Tyr His Leu Lys Leu  
 100 105 110  
 Asp Glu Val Glu Glu Glu Arg Lys Gly Ala Asn Lys Ile Gly Thr Thr  
 115 120 125  
 Lys Lys Gly Ile Gly Pro Ala Tyr Met Asp Lys Ala Ala Arg Ile Gly  
 130 135 140  
 Ile Arg Ile Ala Asp Leu Leu Asp Arg Asp Ala Phe Ala Glu Lys Leu  
 145 150 155 160  
 Glu Arg Asn Leu Glu Glu Lys Asn Arg Leu Leu Glu Lys Met Tyr Glu  
 165 170 175  
 Thr Glu Gly Phe Lys Leu Glu Asp Ile Leu Asp Glu Tyr Tyr Glu Tyr  
 180 185 190  
 Gly Gln Gln Ile Lys Lys Tyr Val Cys Asp Thr Ser Val Val Leu Asn  
 195 200 205  
 Asp Ala Leu Asp Glu Gly Arg Arg Val Leu Phe Glu Gly Ala Gln Gly  
 210 215 220  
 Val Met Leu Asp Ile Asp Gln Gly Thr Tyr Pro Phe Val Thr Ser Ser  
 225 230 235 240  
 Asn Pro Val Ala Gly Gly Val Thr Ile Gly Ser Gly Val Gly Pro Thr  
 245 250 255  
 Lys Ile Lys His Val Val Gly Val Ser Lys Ala Tyr Thr Thr Arg Val  
 260 265 270  
 Gly Asp Gly Pro Phe Pro Thr Glu Leu Lys Asp Glu Ile Gly Asp Gln  
 275 280 285  
 Ile Arg Glu Val Gly Arg Glu Tyr Gly Thr Thr Thr Gly Arg Pro Arg  
 290 295 300  
 Arg Val Gly Trp Phe Asp Ser Val Val Val Arg His Ala Arg Arg Val  
 305 310 315 320  
 Ser Gly Ile Thr Asp Leu Ser Leu Asn Ser Ile Asp Val Leu Ala Gly  
 325 330 335  
 Ile Glu Thr Leu Lys Ile Cys Val Ala Tyr Arg Tyr Lys Gly Glu Ile  
 340 345 350  
 Ile Glu Glu Phe Pro Ala Ser Leu Lys Ala Leu Ala Glu Cys Glu Pro  
 355 360 365

Val	Tyr	Glu	Glu	Met	Pro	Gly	Trp	Thr	Glu	Asp	Ile	Thr	Gly	Ala	Lys
370						375					380				
Ser	Leu	Ser	Glu	Leu	Pro	Glu	Asn	Ala	Arg	His	Tyr	Leu	Glu	Arg	Val
385					390				395					400	
Ser	Gln	Leu	Thr	Gly	Ile	Pro	Leu	Ser	Ile	Phe	Ser	Val	Gly	Pro	Asp
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<210> 15

<211> 899

<212> DNA

<213> *Bacillus subtilis*

<220>

<221> CDS

<222> (101).. (802)

<400> 15

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	Met Ser Val His Ile
	1 5
ggt gct gaa aaa gga caa att gcg gat act gtg ctt ttg ccg gga gat	163
Gly Ala Glu Lys Gly Gln Ile Ala Asp Thr Val Leu Leu Pro Gly Asp	
	10 15 20
cct ctc aga gca aaa ttt att gca gaa acg tat ctt gaa aat gta gaa	211
Pro Leu Arg Ala Lys Phe Ile Ala Glu Thr Tyr Leu Glu Asn Val Glu	
	25 30 35
tgc tac aat gaa gtc aga ggc atg tat gga ttt acg ggt aca tat aaa	259
Cys Tyr Asn Glu Val Arg Gly Met Tyr Gly Phe Thr Gly Thr Tyr Lys	
	40 45 50
ggt aaa aaa atc tca gta caa ggc acg gga atg gga gtt ccg tct att	307
Gly Lys Lys Ile Ser Val Gln Gly Thr Gly Met Gly Val Pro Ser Ile	
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tca att tat gtg aat gaa tta att caa agc tac gat gtg caa aat cta	355



<212> PRT

<213> *Bacillus subtilis*

<400> 16

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			20					25					30		
Leu	Glu	Asn	Val	Glu	Cys	Tyr	Asn	Glu	Val	Arg	Gly	Met	Tyr	Gly	Phe
		35					40					45			
Thr	Gly	Thr	Tyr	Lys	Gly	Lys	Lys	Ile	Ser	Val	Gln	Gly	Thr	Gly	Met
	50					55					60				
Gly	Val	Pro	Ser	Ile	Ser	Ile	Tyr	Val	Asn	Glu	Leu	Ile	Gln	Ser	Tyr
65				70					75					80	
Asp	Val	Gln	Asn	Leu	Ile	Arg	Val	Gly	Ser	Cys	Gly	Ala	Ile	Arg	Lys
			85					90					95		
Asp	Val	Lys	Val	Arg	Asp	Val	Ile	Leu	Ala	Met	Thr	Ser	Ser	Thr	Asp
		100					105						110		
Ser	Gln	Met	Asn	Arg	Val	Ala	Phe	Gly	Ser	Val	Asp	Phe	Ala	Pro	Cys
	115					120					125				
Ala	Asp	Phe	Glu	Leu	Leu	Lys	Asn	Ala	Tyr	Asp	Ala	Ala	Lys	Asp	Lys
	130					135					140				
Gly	Val	Pro	Val	Thr	Val	Gly	Ser	Val	Phe	Thr	Ala	Asp	Gln	Phe	Tyr
145				150					155					160	
Asn	Asp	Asp	Ser	Gln	Ile	Glu	Lys	Leu	Ala	Lys	Tyr	Gly	Val	Leu	Gly
			165					170				175			
Val	Glu	Met	Glu	Thr	Thr	Ala	Leu	Tyr	Thr	Leu	Ala	Ala	Lys	His	Gly
		180					185					190			
Arg	Lys	Ala	Leu	Ser	Ile	Leu	Thr	Val	Ser	Asp	His	Val	Leu	Thr	Gly
	195					200					205				
Glu	Glu	Thr	Thr	Ala	Glu	Glu	Arg	Gln	Thr	Thr	Phe	His	Asp	Met	Ile
	210				215						220				
Glu	Val	Ala	Leu	His	Ser	Val	Ser	Gln							
225				230											